

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT:

(B) NAME: CREATIVE BIOMOLECULES, INC
(C) STREET: 45 SOUTH STREET
(D) STATE: HOPKINTON
10 (E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 01748
(G) TELEPHONE: (508)-435-9001
(H) TELEFAX: (508)-435-0992
(I) TELEX:

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(i) APPLICANT:

(B) NAME: LUDWIG INSTITUTE FOR CANCER RESEARCH
(C) STREET: 1345 AVENUE OF THE AMERICAS
(D) STATE: NY
(E) COUNTRY: USA
20 (F) POSTAL CODE (ZIP): 10105
(G) TELEPHONE: (212)-765-3000
(H) TELEFAX:
(I) TELEX:

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(ii) TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES THEREFOR

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(iii) NUMBER OF SEQUENCES: 15

35

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & THIBEAULT
35 (B) STREET: 53 STATE STREET
(C) CITY: BOSTON
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
45 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: PITCHER, EDMUND R.
(B) REGISTRATION NUMBER: 27,829
55 (C) REFERENCE/DOCKET NUMBER: CRP-097PC

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 248-7000
(B) TELEFAX: (617) 248-7100

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1509 base pairs
(B) TYPE: nucleic acid
5 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1509
15 (D) OTHER INFORMATION: /product= "Human ALK1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | |
|----|---|-----|
| 20 | ATG ACC TTG GGC TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala 1 5 10 15 | 48 |
| 25 | TTG GTG ACC CAG GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val 20 25 30 | 96 |
| 30 | ACC TGC ACG TGT GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly 35 40 45 | 144 |
| 35 | GCC TGG TGC ACA GTA GTG CTG GTG CGG GAG GGG AGG CAC CCC CAG Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln 50 55 60 | 192 |
| 40 | GAA CAT CGG GGC TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg 65 70 75 80 | 240 |
| 45 | CCC ACC GAG TTC GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn 85 90 95 | 288 |
| 50 | CAC AAC GTG TCC CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln 100 105 110 | 336 |
| 55 | CCG GGA ACA GAT GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala 115 120 125 | 384 |
| 60 | TTG CTG GCC CTG GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg 130 135 140 | 432 |
| 65 | CGG AGG CAG GAG AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser 145 150 155 160 | 480 |
| 70 | AGT CTC ATC CTG AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC | 528 |

| | | | |
|----|--|------|--|
| | Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp | | |
| | 165 170 175 | | |
| 5 | CTC CTG GAC AGT GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe | 576 | |
| | 180 185 190 | | |
| 10 | CTG GTG CAG AGG ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val | 624 | |
| | 195 200 205 | | |
| 15 | GGA AAA GGC CGC TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu | 672 | |
| | 210 215 220 | | |
| 20 | AGT GTG GCC GTC AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe | 720 | |
| | 225 230 235 240 | | |
| 25 | CGG GAG ACT GAG ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile | 768 | |
| | 245 250 255 | | |
| 30 | CTA GGC TTC ATC GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln | 816 | |
| | 260 265 270 | | |
| 35 | CTG TGG CTC ATC ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe | 864 | |
| | 275 280 285 | | |
| 40 | CTG CAG AGA CAG ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val | 912 | |
| | 290 295 300 | | |
| 45 | TCC GCG GCA TGC GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr | 960 | |
| | 305 310 315 320 | | |
| 50 | CAG GGC AAA CCA GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val | 1008 | |
| | 325 330 335 | | |
| 55 | CTG GTC AAG AGC AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala | 1056 | |
| | 340 345 350 | | |
| 60 | GTG ATG CAC TCA CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro | 1104 | |
| | 355 360 365 | | |
| 65 | AGA GTG GGC ACC AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln | 1152 | |
| | 370 375 380 | | |
| 70 | ATC CGC ACG GAC TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC ATC TGG GCC Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala | 1200 | |
| | 385 390 395 400 | | |
| 75 | TTT GGC CTG GTG CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC | 1248 | |

Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
405 410 415

ATC GTG GAG GAC TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC 1296
Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
420 425 430

CCC AGC TTT GAG GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC 1344
Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
10 435 440 445

CCC ACC ATC CCT AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA 1392
Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
450 455 460

GCT CAG ATG ATG CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC 1440
Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
465 470 475 480

ACC GCG CTG CGG ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA 1488
Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
485 490 495

GAG AAG CCT AAA GTG ATT CAA 1509
25 Glu Lys Pro Lys Val Ile Gln
500

(2) INFORMATION FOR SEQ ID NO:2:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

40 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
1 5 10 15

Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
20 25 30

45 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
35 40 45

50 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
50 55 60

Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
65 70 75 80

55 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
85 90 95

His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
100 105 110

Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
115 120 125

5 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
130 135 140

Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
145 150 155 160

10 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
165 170 175

Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
180 185 190

15 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
195 200 205

Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
20 210 215 220

Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
225 230 235 240

25 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
245 250 255

Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
260 265 270

30 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
275 280 285

Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
35 290 295 300

Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
305 310 315 320

40 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
325 330 335

Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
340 345 350

45 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
355 360 365

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
50 370 375 380

Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
385 390 395 400

55 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
405 410 415

Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
60 420 425 430

Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
435 440 445
5 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
450 455 460
Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
465 470 475 480
10 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
485 490 495
Glu Lys Pro Lys Val Ile Gln
500
15

(2) INFORMATION FOR SEQ ID NO:3:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2724 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
25 (ii) MOLECULE TYPE: cDNA

30 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 104..1633
(D) OTHER INFORMATION: /product= "Human ALK2"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAAG 60
GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA 115
Mét Val Asp Gly
40 GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT 163
Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
5 10 15 20
45 ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG 211
Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
25 30 35
50 TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG 259
Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
40 45 50
55 TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA 307
Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
55 60 65
60 GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG 355
Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
60 70 75 80

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|----|---|------|
| | CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn 85 90 95 100 | 403 |
| 5 | AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly 105 110 115 | 451 |
| 10 | ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val 120 125 130 | 499 |
| 15 | TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys 135 140 145 | 547 |
| 20 | TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr 150 155 160 | 595 |
| 25 | GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu 165 170 175 180 | 643 |
| 30 | GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu 185 190 195 | 691 |
| 35 | CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu 200 205 210 | 739 |
| 40 | TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln 215 220 225 | 787 |
| 45 | GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser 230 235 240 | 835 |
| 50 | TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu 245 250 255 260 | 883 |
| 55 | AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACA TCA AGA CAC TCC AGT Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser 265 270 275 | 931 |
| 60 | ACC CAG CTG TGG TTA ATT ACA CAT TAT CAT GAA ATG GGA TCG TTG TAC Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly Ser Leu Tyr 280 285 290 | 979 |
| | GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GGT AGC TGC CTT CGA ATA Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile 295 300 305 | 1027 |
| | GTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe 310 315 320 | 1075 |

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|----|---|-------------------------------|
| | GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys 325 330 335 340 | 1123 |
| 5 | AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly 345 350 355 | 1171 |
| 10 | CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn 360 365 370 | 1219 |
| 15 | AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp 375 380 385 | 1267 |
| 20 | GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile 390 395 400 | 1315 |
| 25 | TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser 405 410 415 420 | 1363 |
| 30 | AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro 425 430 435 | 1411 |
| 35 | AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln 440 445 450 | 1459 |
| 40 | CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr 455 460 465 | 1507 |
| 45 | TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala 470 475 480 | 1555 |
| 50 | AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn 485 490 495 500 | 1603 |
| 55 | TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA Ser Leu Asp Lys Leu Lys Thr Asp Cys 505 510 | 1650 |
| 60 | GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGAC CTAATGCTGG CCTGACTGGT TGTCAGAACATCT GTCTCCCTCC CCAAATGGCT GCTTGACAA GGCAGACGTC GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCCTA ACCTCGCTCG ATGACTGTGA ACTGGGCATT TCACGAAC TG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGCAT TAAGTCAGTG GCTTTGCATA GCTTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT | 1710 1770 1830 1890 1950 2010 |

GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTCTTT ATTGCACTAG GAATTCTTG 2070
CATTCCCTAAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTGCCAA AATGTTGGCT 2130
5 GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA CAAAATGTAA 2190
TGTCAAGACTT TGCTGCATTT TACACATGTG CTGATGTTA CAATGATGCC GAACATTAGG 2250
10 AATTGTTTAT ACACAACCTT GCAAATTATT TATTACTTGT GCACTTAGTA GTTTTACAA 2310
AACTGCTTTG TGCAATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT TATTACAGAA 2370
15 ATGTTTTAA CACTATACTC TAAAATGGAC ATTTTCTTT ATTATCAGTT AAAATCACAT 2430
TTTAAGTGCT TCACATTGTT ATGTGTGTAG ACTGTAACCTT TTTTCAGTT CATATGCAGA 2490
ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA GAAGCAAAGA 2550
20 TTTCAGTAGA ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTCCTTC AGAATTATCC 2610
ATTACGTGCA TTTAAACTCT GCCAGAAAAA ATAACATTATT TTGTTTAAT CTACTTTTG 2670
TATTAGTAG TTATTTGTAT AAATAAATA AACTGTTTC AAGTCAAAAA AAAA 2724
25

(2) INFORMATION FOR SEQ ID NO:4:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 509 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
1 5 10 15
40 Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
20 25 30
Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
45 35 40 45
Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
50 55 60
50 Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
65 70 75 80
Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
85 90 95
55 Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
100 105 110
60 Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
115 120 125

Leu Ser Val Val Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val
130 135 140

5 Ala Leu Arg Lys Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg
145 150 155 160

Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
165 170 175

10 Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
180 185 190

Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
15 195 200 205

Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
210 215 220

20 Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
225 230 235 240

Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
245 250 255

25 Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
260 265 270

Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
30 275 280 285

Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
290 295 300

35 Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
305 310 315 320

Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
325 330 335

40 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
340 345 350

Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
45 355 360 365

Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
370 375 380

50 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
385 390 395 400

Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
405 410 415

55 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
420 425 430

Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
60 435 440 445

Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
450 455 460

5 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
465 470 475 480

Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
485 490 495

10 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
500 505

15 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

20 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 310..1908
(D) OTHER INFORMATION: /product= "Human ALK3"

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35 GCTCCCGGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT 60
CAGTTAATA CTGTCTTGGA ATTCACTGAGA TGGAAGCATA GGTCAAAGCT GTTGGAGAA 120
AATCAGAAAGT ACAGTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG 180
40 TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA 240
TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC 300
AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC 348
45 Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala
1 5 10

TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG 396
Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met
15 20 25

50 CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA 444
Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu
30 35 40 45

55 AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC 492
Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys
50 55 60

60 TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC AGA TGC ATA 540

| | | | |
|----|---|--|------|
| | Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile | | |
| | 65 70 75 | | |
| 5 | ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu 80 85 90 | | 588 |
| 10 | ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln 95 100 105 | | 636 |
| 15 | TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys 110 115 120 125 | | 684 |
| 20 | CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Val 130 135 140 | | 732 |
| 25 | GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC Val Ile Gly Pro Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu 145 150 155 | | 780 |
| 30 | ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys 160 165 170 | | 828 |
| 35 | TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr 175 180 185 | | 876 |
| 40 | AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser 190 195 200 205 | | 924 |
| 45 | CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly 210 215 220 | | 972 |
| 50 | CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val 225 230 235 | | 1020 |
| 55 | CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp 240 245 250 | | 1068 |
| 60 | CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala 255 260 265 | | 1116 |
| 65 | AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His 270 275 280 285 | | 1164 |
| 70 | GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser 290 295 300 | | 1212 |
| 75 | TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC | | 1260 |

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200660

| | | | |
|----|---|--|------|
| | Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu | | |
| | 305 310 315 | | |
| 5 | TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys 320 325 330 | | 1308 |
| 10 | TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile 335 340 345 | | 1356 |
| 15 | TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser 350 355 360 365 | | 1404 |
| 20 | AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG Lys Asn Ile Leu Ile Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu 370 375 380 | | 1452 |
| 25 | GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro 385 390 395 | | 1500 |
| 30 | TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu 400 405 410 | | 1548 |
| 35 | GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp 415 420 425 | | 1596 |
| 40 | ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile 430 435 440 445 | | 1644 |
| 45 | ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val 450 455 460 | | 1692 |
| 50 | CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys 465 470 475 | | 1740 |
| 55 | CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu 480 485 490 | | 1788 |
| 60 | CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala 495 500 505 | | 1836 |
| | TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT Ser Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val 510 515 520 525 | | 1884 |
| | GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAAACTCT Glu Ser Gln Asp Val Lys Ile 530 | | 1935 |
| | AGACTGCAAG AACTGTTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT | | 1995 |

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0905201906150
AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTCACAG GCTGCTAATA TTAAACCTTT 2055
CAGTACTCTT ATTAGGATAC AAGCTGGAA CTTCTAAACA CTTCATTCTT TATATATGGA 2115
5 CAGCTTTATT TTAAATGTGG TTTTGATGC CTTTTTTAA GTGGGTTTT ATGAACGTCA 2175
TCAAGACTTC AACCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTT 2235
10 ATAAAACGGT CCTTCTGTG AAAGCCTAA GAAGATAAAAT GAGCGCAGCA GAGATGGAGA 2295
AATAGACTTT GCCTTTTACCGC TGAGACATTC AGTTCGTTTG TATTCTACCT TTGTAAAACA 2355
15 GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTA TGATAGTTG TCCTGTGTCC 2415
TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCTCTGC TGCCATTGA 2475
ATTAGAAGAA AATAATTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTGTG 2535
20 CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TTACTTTGCA 2595
AGTGAGATAG CTTCCCCACC AGCTTATTT TTTAACATGA AAGCTGATGC CAAGGCCAAA 2655
25 AGAAGTTAA AGCATCTGTA AATTGGACT GTTTCCCTTC AACCAACCATT TTTTTGTGG 2715
TTATTATTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC 2775
ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCCT GCATTGATA GCAATGTAAG 2835
30 TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTAA 2895
TATTTGTGT ATAATGTGCT TTATTGCAA ATCACCC 2932

35 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids
(B) TYPE: amino acid
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

45 Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe
1 5 10 15
Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
50 20 25 30
Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val
35 40 45
55 Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser
50 55 60
Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly
65 70 75 80
60

His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu
85 90 95

Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp
5 100 105 110

Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn
115 120 125

10 Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly
130 135 140

Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu Ile Ser Met
145 150 155 160

15 Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr
165 170 175

Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn Arg Asp
20 180 185 190

Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
195 200 205

25 Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu
210 215 220

Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
225 230 235 240

30 Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
245 250 255

35 Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
260 265 270

Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
275 280 285

40 Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
290 295 300

Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
305 310 315 320

45 Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
325 330 335

50 Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
340 345 350

Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
355 360 365

55 Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
370 375 380

Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu Asn Thr
385 390 395 400

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
405 410 415

Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
5 420 425 430

Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
435 440 445

Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
10 450 455 460

Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
15 465 470 475 480

Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
485 490 495

Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
20 500 505 510

Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
515 520 525

Asp Val Lys Ile
25 530

(2) INFORMATION FOR SEQ ID NO:7:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1952 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 187..1695
(D) OTHER INFORMATION: /product= "Murine ALK6"

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCGGCGGC AGAACGTTGCC GGCGTGGTGC TCGTAGTGAG GGCGCGGAGG ACCCGGGACC 60
50 TGGGAAGCGG CGGCAGGGTTA ACTTCGGCTG AATCACAAAC 187..1695 ATTTGGCGCT GAGCTATGAC 120
AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT 180
55 GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG 228
Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys
1 5 10

AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA 276
Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu
60 15 20 25 30

| | | |
|----|---|-----|
| | CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile 35 40 45 | 324 |
| 5 | TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser 50 55 60 | 372 |
| 10 | GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp 65 70 75 | 420 |
| 15 | TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu 80 85 90 | 468 |
| 20 | TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu 95 100 105 110 | 516 |
| 25 | CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys 115 120 125 | 564 |
| 30 | GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile 130 135 140 | 612 |
| 35 | ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg 145 150 155 | 660 |
| 40 | TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu 160 165 170 | 708 |
| 45 | TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser 175 180 185 190 | 756 |
| 50 | GCG CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met 195 200 205 | 804 |
| 55 | GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys 210 215 220 | 852 |
| 60 | TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu 225 230 235 | 900 |
| | GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg 240 245 250 | 948 |
| | CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly 255 260 265 270 | 996 |

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|----|---|------|
| | TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser 275 280 285 | 1044 |
| 5 | CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu 290 295 300 | 1092 |
| 10 | AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu 305 310 315 | 1140 |
| 15 | ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys 320 325 330 | 1188 |
| 20 | AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp 335 340 345 350 | 1236 |
| 25 | CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile 355 360 365 | 1284 |
| 30 | CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val 370 375 380 | 1332 |
| 35 | CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala 385 390 395 | 1380 |
| 40 | GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys 400 405 410 | 1428 |
| 45 | GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu 415 420 425 430 | 1476 |
| 50 | GTC CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met 435 440 445 | 1524 |
| 55 | AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys 450 455 460 | 1572 |
| 60 | CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro 465 470 475 | 1620 |
| 65 | GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met 480 485 490 | 1668 |
| 70 | TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGAGA CAGAGCAAGA Ser Glu Ser Gln Asp Ile Lys Leu | 1722 |
| 75 | 495 500 | |

D E S C R I P T I O N

ATTCACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCC AGTGAGTTCA 1782
5 GACTTCCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT 1842
CATGGCTTTC TGAGGAGGAG AAACTGTTG GGTAACTTGT TCAAGATATG ATGCATGTTG 1902
CTTTCTAAGA AAGCCCTGTA TTTGAATTA CCATTTTTT ATAAAAAAA 1952

10 (2) INFORMATION FOR SEQ ID NO:8:

(i). SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 502 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Leu Leu Arg Ser Ser Gly Leu Asn Val Gly Thr Lys Lys Glu
1 5 10 15

25 Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys
20 25 30

Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser
35 40 45

30 Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met
50 55 60

35 Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln
65 70 75 80

Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys
85 90 95

40 Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
100 105 110

Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu
115 120 125

45 Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
130 135 140

50 Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser
145 150 155 160

Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
165 170 175

55 Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu
180 185 190

Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
195 200 205

Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg
210 215 220

5 Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser
225 230 235 240

Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu
245 250 255

10 Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp
260 265 270

Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr
275 280 285

15 Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
290 295 300

20 Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
305 310 315 320

Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys
325 330 335

25 Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
340 345 350

Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
355 360 365

30 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp
370 375 380

35 Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met
385 390 395 400

Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser
405 410 415

40 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro
420 425 430

Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys
435 440 445

45 Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg
450 455 460

50 Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser
465 470 475 480

Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu
485 490 495

55 Ser Gln Asp Ile Lys Leu
500

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1822 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

10 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 49..1341
(D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
/product= "OP1"
/evidence= EXPERIMENTAL
/standard_name= "OP1"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20 GGTGCGGGCC CGGAGCCCGG AGCCCCGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG
Met His Val
1 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA
25 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
5 10 15
CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC
30 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
20 25 30 35
GAG GTG CAC TCG AGC TTC ATC CAC CCG CGC CTC CGC AGC CAG GAG CGG
35 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
40 45 50
CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC
35 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
55 60 65
40 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG
Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
70 75 80
45 CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC
Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Pro Gly
85 90 95
50 GGC CAG GGC TTC TCC TAC CCC TAC AAG GGC GTC TTC AGT ACC CAG GGC
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
100 105 110 115
55 CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GGC GAC
Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
120 125 130
55 ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC
Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
135 140 145
60 CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC

| | | | |
|----|---|--|------|
| | His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile | | |
| | 150 155 160 | | |
| 5 | CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp 165 170 175 | | 585 |
| 10 | TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr 180 185 190 195 | | 633 |
| | CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu 200 205 210 | | 681 |
| 15 | GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp 215 220 225 | | 729 |
| 20 | ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu 230 235 240 | | 777 |
| 25 | GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro 245 250 255 | | 825 |
| 30 | AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro 260 265 270 275 | | 873 |
| | TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile 280 285 290 | | 921 |
| 35 | CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro 295 300 305 | | 969 |
| 40 | AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser 310 315 320 | | 1017 |
| 45 | AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe 325 330 335 | | 1065 |
| 50 | CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala 340 345 350 355 | | 1113 |
| | GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met 360 365 370 | | 1161 |
| 55 | AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375 380 385 | | 1209 |
| 60 | CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC | | 1257 |

Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
390 395 400

5 ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA 1305
Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
405 410 415

TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC 1351
Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
10 420 425 430

GAGAATTCAAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG 1411

15 GAACCAGCAG ACCAACTGCC TTTTGAGA CCTTCCCCCTC CCTATCCCCA ACTTTAAAGG 1471

TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTG ATCAGTTTT CAGTGGCAGC 1531

ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAAACAC 1591

20 GCATAAAAGAA AAATGGCCGG GCCAGGTCAAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT 1651

CGTTTCCAGA GGTAAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG 1711

25 GGCGTGGCAA GGGGTGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC 1771

CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A 1822

(2) INFORMATION FOR SEQ ID NO:10:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

40 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
1 5 10 15

Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
45 20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
35 40 45

50 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
50 55 60

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
65 70 75 80

55 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly
85 90 95

Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
60 100 105 110

Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
115 120 125

Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
5 130 135 140

Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
145 150 155 160

Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
10 165 170 175

Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
180 185 190

Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
15 195 200 205

Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
20 210 215 220

Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
225 230 235 240

His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
25 245 250 255

Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
30 260 265 270

Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
275 280 285

Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
35 290 295 300

Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
305 310 315 320

Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
40 325 330 335

Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
45 340 345 350

Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
355 360 365

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
50 370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
55 405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
60 420 425 430

(2) INFORMATION FOR SEQ ID NO:11:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /label= OPX

20 /note= "Each Xaa is independently selected from
a group of one or more specified amino acids
as defined in the specification"

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30 Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
1 5 10 15

35 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
20 25 30

40 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
35 40 45

45 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
50 55 60

55 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
65 70 75 80

60 Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
85 90 95

65 Xaa Ala Cys Gly Cys His
100

(2) INFORMATION FOR SEQ ID NO:12:

70 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

75 (ii) MOLECULE TYPE: cDNA

80 (iii) HYPOTHETICAL: NO

85 (iv) ANTI-SENSE: NO

90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

28

GCGGATCCTG TTGTGAAGGN AATATGTG

(2) INFORMATION FOR SEQ ID NO:13:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

24

GCGATCCGTC GCAGTCAAAA TTTT

(2) INFORMATION FOR SEQ ID NO:14:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

35 (iii) HYPOTHETICAL: NO

35 (iv) ANTI-SENSE: NO

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

26

GCGGATCCGC GATATATTAA AAGCAA

(2) INFORMATION FOR SEQ ID NO:15:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

55 (iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

20

60 CGGAATTCTG GTGCCATATA